

#4



SEQUENCE LISTING

<110> Arnaut, Greta
Boets, Anneke
Vanneste, Stijn
Van Rie, Jeroen
Van Houdt, Sara

<120> Novel Bacillus thuringiensis insecticidal proteins

<130> 58764.000036

<140> US 10/040,906

<141> 2002-01-09

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<170> PatentIn version 3.1

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<212> DNA

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<221> CDS

<222> (1)..(1896)

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tct atc tgg tgc ttg ttt aaa tat caa agc ctt cta gta tct tct ggc Ser Ile Trp Ser Leu Phe Lys Tyr Gln Ser Leu Leu Val Ser Ser Gly 260 265 270			816
gct aat tta tat gca agc ggt agt gga cca cag cag act caa tca ttt Ala Asn Leu Tyr Ala Ser Gly Ser Gly Pro Gln Gln Thr Gln Ser Phe 275 280 285			864
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 50 55 60

Val Gly Ser Leu Ile Gly Lys Arg Ile Leu Ser Glu Leu Trp Gly Leu
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Val Asn Ala Glu Leu Glu Gly Leu Gln Ala Asn Ile Arg Glu Phe Asn
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Gln Gln Val Asp Asn Phe Leu Asn Pro Thr Gln Asn Pro Val Pro Leu
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185

190

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Thr Ile Gln Glu Glu Trp Met Glu Trp Lys Lys Asp Asn His Ser Leu	
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Tyr Val Asp Pro Ile Val Gly Thr Val Ala Ser Phe Leu Leu Lys Lys	
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Phe Ala Gln Ala Ala Asn Leu His Leu Ser Phe Ile Arg Asp Val Ile
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Leu Asn Ala Asp Glu Trp Gly Ile Ser Ala Ala Thr Leu Arg Thr Tyr
195 200 205

Gln Asn His Leu Arg Asn Tyr Thr Arg Asp Tyr Ser Asn Tyr Cys Ile
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Asn Thr Tyr Gln Thr Ala Phe Arg Gly Leu Asn Thr Arg Leu His Asp
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Pro Asn Ile Val Gly Leu Pro Gly Thr Thr Thr Thr His Ala Leu Leu
 325 330 335

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Leu Thr Pro Phe Val Arg Ser Trp Leu Asp Ser Gly Ser Asp Arg Gly
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Phe Pro Asp Tyr Phe Ile Arg Asn Ile Ser Gly Val Pro Leu Val Val
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Arg Asn Glu Asp Leu Arg Arg Pro Leu His Tyr Asn Gln Ile Arg Asn
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Ser Val His Asn Arg Lys Asn Asn Ile Tyr Ala Val His Glu Asn Gly
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Thr Met Ile His Leu Ala Pro Glu Asp Tyr Thr Gly Phe Thr Ile Ser
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Pro Ile His Ala Thr Gln Val Asn Asn Gln Thr Arg Thr Phe Ile Ser
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Tyr Val Ser Pro Ile Val Gly Thr Ile Ala Ser Phe Leu Leu Lys Lys
50 55 60
ata gga ggg ctt ata gga aaa aga ata tta agt gag tta aag aat tta 240
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115 120 125	
cga caa gtg gac aat ttt tta aac cca aat caa aac cct gcc cct tta	432
Arg Gln Val Asp Asn Phe Leu Asn Pro Asn Gln Asn Pro Ala Pro Leu	
130 135 140	
gca ata att gat tcg gtt aat aca ttg caa caa tta ttc cta agt aga	480
Ala Ile Ile Asp Ser Val Asn Thr Leu Gln Gln Leu Phe Leu Ser Arg	
145 150 155 160	
tta ccc cag ttc cag ata caa cgc tat cag cta tta tta tta cct tta	528
Leu Pro Gln Phe Gln Ile Gln Arg Tyr Gln Leu Leu Leu Leu Pro Leu	
165 170 175	
ttt gca caa gca gcc aat tta cac ctt tct ttt att aga gac gtt att	576
Phe Ala Gln Ala Ala Asn Leu His Leu Ser Phe Ile Arg Asp Val Ile	
180 185 190	
ctt aat gca gat gaa tgg gga ata cca gct gca acg gtg cgc aca tat	624
Leu Asn Ala Asp Glu Trp Gly Ile Pro Ala Ala Thr Val Arg Thr Tyr	
195 200 205	
aga gag cac cta caa aga tat aca cgc gaa tac tcc aat tat tgt ata	672
Arg Glu His Leu Gln Arg Tyr Thr Arg Glu Tyr Ser Asn Tyr Cys Ile	
210 215 220	
aat acg tat caa act gcg ttt aga ggg tta aat gcc act tta cac gat	720
Asn Thr Tyr Gln Thr Ala Phe Arg Gly Leu Asn Ala Thr Leu His Asp	
225 230 235 240	
ttt cta gaa ttt aga aca tat atg ttt tta aat gta tta gac tat gta	768
Phe Leu Glu Phe Arg Thr Tyr Met Phe Leu Asn Val Leu Asp Tyr Val	
245 250 255	
tct atc tgg tcg ttg ttt aaa tat cag agc ctt ctg gta tcc tct ggc	816
Ser Ile Trp Ser Leu Phe Lys Tyr Gln Ser Leu Leu Val Ser Ser Gly	
260 265 270	
gct aat tta tat gcg agt ggt agt gga gta aca aat aga caa tca ttt	864
Ala Asn Leu Tyr Ala Ser Gly Ser Gly Val Thr Asn Arg Gln Ser Phe	
275 280 285	
act gca caa gac tgg cca ttt tta aat tct ctt ttc caa gtt aat caa	912
Thr Ala Gln Asp Trp Pro Phe Leu Asn Ser Leu Phe Gln Val Asn Gln	
290 295 300	
aat tat gta tta aca ggt atg aat ggt tat agg tat act tta agt tct	960
Asn Tyr Val Leu Thr Gly Met Asn Gly Tyr Arg Tyr Thr Leu Ser Ser	
305 310 315 320	
gtt ttt ggt aca aat caa aca ata cat tct gtt agg agt aat tat agg	1008
Val Phe Gly Thr Asn Gln Thr Ile His Ser Val Arg Ser Asn Tyr Arg	

325	330	335	
ggc ggg gtt tca tct ggt tac att Gly Gly Val Ser Ser Gly Tyr Ile 340	gga gtt aat ctt agt gaa ggt gac Gly Val Asn Leu Ser Glu Gly Asp 345		1056
caa aat ttt agt tgt agt aca ttt ttg gat cct tta gaa aca ccg ttt Gln Asn Phe Ser Cys Ser Thr Phe Leu Asp Pro Leu Glu Thr Pro Phe 355			1104
att aga agt tgg ctg gat tca ggt agc gat gat ggc ttt aat tgg agt Ile Arg Ser Trp Leu Asp Ser Gly Ser Asp Asp Gly Phe Asn Trp Ser 370			1152
aca gga gtc ttt aca aca act att ggt tta cct act tgt agc att ttt Thr Gly Val Phe Thr Thr Ile Gly Leu Pro Thr Cys Ser Ile Phe 385			1200
tgg cct cgt ggt aac tcg aac tat ttt cca gat tat ttt ata cga aat Trp Pro Arg Gly Asn Ser Asn Tyr Phe Pro Asp Tyr Phe Ile Arg Asn 405			1248
att tct ggt gtc gtt ggt cgt ctt agg aac gaa gat tta aga aga cca Ile Ser Gly Val Val Gly Arg Leu Arg Asn Glu Asp Leu Arg Arg Pro 420			1296
cta tat ttt aat gag ata aga aat ata gta gga aat aac aat cca ccg Leu Tyr Phe Asn Glu Ile Arg Asn Ile Val Gly Asn Asn Asn Pro Pro 435			1344
gca act gga tcg tta tca gtc gcc agc cta gtc tct gtg cat aac aga Ala Thr Gly Ser Leu Ser Val Ala Ser Leu Val Ser Val His Asn Arg 450			1392
aaa aat aat att tat gct gct cat gaa aat ggt act atg att cat ttg Lys Asn Asn Ile Tyr Ala Ala His Glu Asn Gly Thr Met Ile His Leu 465			1440
gca ccg gaa gat tat aca ggt ttc aca atg tca cca ata cat gca act Ala Pro Glu Asp Tyr Thr Gly Phe Thr Met Ser Pro Ile His Ala Thr 485			1488
caa gta aat aat caa aca cga aca ttt att tcc gag aaa tta gga aac Gln Val Asn Asn Gln Thr Arg Thr Phe Ile Ser Glu Lys Leu Gly Asn 500			1536
caa ggt gat tcc ttg aga ttt gaa caa aca aat aca acg gct cga tac Gln Gly Asp Ser Leu Arg Phe Glu Gln Thr Asn Thr Thr Ala Arg Tyr 515			1584
aca ttt aga ggg aat gga aat agt tac aat ctt tat tta aga gta tct Thr Phe Arg Gly Asn Gly Asn Ser Tyr Asn Leu Tyr Leu Arg Val Ser 530			1632
tca cta gga aat tcc aca att cga gtt act ata aac ggt aga gtt tat Ser Leu Gly Asn Ser Thr Ile Arg Val Thr Ile Asn Gly Arg Val Tyr 545			1680
act gtt tca aac gtc aat act act aca aat aac gat gga gtt gtt gat Thr Val Ser Asn Val Asn Thr Thr Thr Asn Asn Asp Gly Val Val Asp 565			1728

aat ggc gct cgt ttt tca gat att aat ata ggt aat gta gtg gca agt 1776
 Asn Gly Ala Arg Phe Ser Asp Ile Asn Ile Gly Asn Val Val Ala Ser
 580 585 590

gct aat act aat ata cca tta gat ata aat gta aca ttt aac tct ggt 1824
 Ala Asn Thr Asn Ile Pro Leu Asp Ile Asn Val Thr Phe Asn Ser Gly
 595 600 605

acg caa ttt gag ctt atg aat att atg ttt gtt cca act aat att cca 1872
 Thr Gln Phe Glu Leu Met Asn Ile Met Phe Val Pro Thr Asn Ile Pro
 610 615 620

cca att tat taa 1884
 Pro Ile Tyr
 625

<210> 6
 <211> 627
 <212> PRT
 <213> Bacillus thuringiensis

<400> 6

Met Asn Asn Val Leu Asn Ser Glu Arg Thr Thr Lys Cys Gly Ala Tyr
 1 5 10 15

Asn Val Val Ala His Asp Pro Phe Ser Phe Glu His Lys Ser Leu Asp
 20 25 30

Thr Ile Gln Lys Glu Trp Met Glu Trp Lys Arg Thr Asp His Ser Leu
 35 40 45

Tyr Val Ser Pro Ile Val Gly Thr Ile Ala Ser Phe Leu Leu Lys Lys
 50 55 60

Ile Gly Gly Leu Ile Gly Lys Arg Ile Leu Ser Glu Leu Lys Asn Leu
 65 70 75 80

Ile Phe Pro Ser Gly Ser Ile Glu Ser Met Gln Asp Ile Leu Arg Gly
 85 90 95

Ala Glu Gln Phe Leu Asn Gln Arg Leu Asp Ala Asp Thr Phe Ser Arg
 100 105 110

Val Glu Ala Glu Leu Arg Gly Leu Gln Ala Asn Val Glu Glu Phe Asn
 115 120 125

Arg Gln Val Asp Asn Phe Leu Asn Pro Asn Gln Asn Pro Ala Pro Leu
 130 135 140

Ala Ile Ile Asp Ser Val Asn Thr Leu Gln Gln Leu Phe Leu Ser Arg
 145 150 155 160

Leu Pro Gln Phe Gln Ile Gln Arg Tyr Gln Leu Leu Leu Leu Pro Leu
 165 170 175

Phe Ala Gln Ala Ala Asn Leu His Leu Ser Phe Ile Arg Asp Val Ile
 180 185 190

Leu Asn Ala Asp Glu Trp Gly Ile Pro Ala Ala Thr Val Arg Thr Tyr
 195 200 205

Arg Glu His Leu Gln Arg Tyr Thr Arg Glu Tyr Ser Asn Tyr Cys Ile
 210 215 220

Asn Thr Tyr Gln Thr Ala Phe Arg Gly Leu Asn Ala Thr Leu His Asp
 225 230 235 240

Phe Leu Glu Phe Arg Thr Tyr Met Phe Leu Asn Val Leu Asp Tyr Val
 245 250 255

Ser Ile Trp Ser Leu Phe Lys Tyr Gln Ser Leu Leu Val Ser Ser Gly
 260 265 270

Ala Asn Leu Tyr Ala Ser Gly Ser Gly Val Thr Asn Arg Gln Ser Phe
 275 280 285

Thr Ala Gln Asp Trp Pro Phe Leu Asn Ser Leu Phe Gln Val Asn Gln
 290 295 300

Asn Tyr Val Leu Thr Gly Met Asn Gly Tyr Arg Tyr Thr Leu Ser Ser
 305 310 315 320

Val Phe Gly Thr Asn Gln Thr Ile His Ser Val Arg Ser Asn Tyr Arg
 325 330 335

Gly Gly Val Ser Ser Gly Tyr Ile Gly Val Asn Leu Ser Glu Gly Asp
 340 345 350

Gln Asn Phe Ser Cys Ser Thr Phe Leu Asp Pro Leu Glu Thr Pro Phe
 355 360 365

Ile Arg Ser Trp Leu Asp Ser Gly Ser Asp Asp Gly Phe Asn Trp Ser
 370 375 380

Thr Gly Val Phe Thr Thr Thr Ile Gly Leu Pro Thr Cys Ser Ile Phe

385		390		395		400
Trp Pro Arg Gly	Asn Ser Asn Tyr Phe	Pro Asp Tyr Phe Ile Arg Asn				
	405	410			415	
Ile Ser Gly Val Val Gly Arg Leu Arg Asn Glu Asp Leu Arg Arg Pro						
	420	425			430	
Leu Tyr Phe Asn Glu Ile Arg Asn Ile Val Gly Asn Asn Asn Pro Pro						
	435	440			445	
Ala Thr Gly Ser Leu Ser Val Ala Ser Leu Val Ser Val His Asn Arg						
	450	455			460	
Lys Asn Asn Ile Tyr Ala Ala His Glu Asn Gly Thr Met Ile His Leu						
	465	470			475	480
Ala Pro Glu Asp Tyr Thr Gly Phe Thr Met Ser Pro Ile His Ala Thr						
	485	490			495	
Gln Val Asn Asn Gln Thr Arg Thr Phe Ile Ser Glu Lys Leu Gly Asn						
	500	505			510	
Gln Gly Asp Ser Leu Arg Phe Glu Gln Thr Asn Thr Thr Ala Arg Tyr						
	515	520			525	
Thr Phe Arg Gly Asn Gly Asn Ser Tyr Asn Leu Tyr Leu Arg Val Ser						
	530	535			540	
Ser Leu Gly Asn Ser Thr Ile Arg Val Thr Ile Asn Gly Arg Val Tyr						
	545	550			555	560
Thr Val Ser Asn Val Asn Thr Thr Thr Asn Asn Asp Gly Val Val Asp						
	565	570			575	
Asn Gly Ala Arg Phe Ser Asp Ile Asn Ile Gly Asn Val Val Ala Ser						
	580	585			590	
Ala Asn Thr Asn Ile Pro Leu Asp Ile Asn Val Thr Phe Asn Ser Gly						
	595	600			605	
Thr Gln Phe Glu Leu Met Asn Ile Met Phe Val Pro Thr Asn Ile Pro						
	610	615			620	
Pro Ile Tyr						
625						

<210> 7
 <211> 1910
 <212> DNA
 <213> Unknown

<220>
 <223> artificial cry2Ae DNA sequence for expression in cotton

<220>
 <221> CDS
 <222> (3)..(1901)
 <223>

<400> 7
 cc atg gct aac aac gtt ctt aac aac ggt agg act act att tgc gat 47
 Met Ala Asn Asn Val Leu Asn Asn Gly Arg Thr Thr Ile Cys Asp
 1 5 10 15
 gca tac aac gtt gtt gct cat gat cct ttc tct ttc gag cat aag tct 95
 Ala Tyr Asn Val Val Ala His Asp Pro Phe Ser Phe Glu His Lys Ser
 20 25 30
 ctt gat aca att agg aag gag tgg atg gag tgg aag agg act gat cat 143
 Leu Asp Thr Ile Arg Lys Glu Trp Met Glu Trp Lys Arg Thr Asp His
 35 40 45
 tct ctt tac gtt gct cct att gtt ggt act gtt tct tct ttc ctt ctt 191
 Ser Leu Tyr Val Ala Pro Ile Val Gly Thr Val Ser Ser Phe Leu Leu
 50 55 60
 aag aag gtt ggt tct ctt atc ggt aag agg atc ctt tct gag ctt tgg 239
 Lys Lys Val Gly Ser Leu Ile Gly Lys Arg Ile Leu Ser Glu Leu Trp
 65 70 75
 ggt ctt atc ttc cct tct ggt tct act aac ctt atg caa gat att ctt 287
 Gly Leu Ile Phe Pro Ser Gly Ser Thr Asn Leu Met Gln Asp Ile Leu
 80 85 90 95
 agg gag act gaa caa ttc ctt aac cag agg ctt aac act gat act ctt 335
 Arg Glu Thr Glu Gln Phe Leu Asn Gln Arg Leu Asn Thr Asp Thr Leu
 100 105 110
 gct agg gtt aac gct gag ctt gag ggt ctt caa gct aac att agg gaa 383
 Ala Arg Val Asn Ala Glu Leu Glu Gly Leu Gln Ala Asn Ile Arg Glu
 115 120 125
 ttc aac cag caa gtt gat aac ttc ctt aac cct act caa aac cct gtt 431
 Phe Asn Gln Gln Val Asp Asn Phe Leu Asn Pro Thr Gln Asn Pro Val
 130 135 140
 cct ctt tct att act tct tct gtt aac act atg caa caa ctt ttc ctt 479
 Pro Leu Ser Ile Thr Ser Ser Val Asn Thr Met Gln Gln Leu Phe Leu
 145 150 155
 aac agg ctt cct caa ttc agg gtt caa ggt tac caa ctt ctt ctt ctt 527
 Asn Arg Leu Pro Gln Phe Arg Val Gln Gly Tyr Gln Leu Leu Leu Leu
 160 165 170 175

cct ctt ttc gct caa gct gct aac atg cac cta agc ttc att agg gat	575
Pro Leu Phe Ala Gln Ala Ala Asn Met His Leu Ser Phe Ile Arg Asp	
180 185 190	
ggt gtt ctt aac gct gat gag tgg ggt att tct gct gct act ctt agg	623
Val Val Leu Asn Ala Asp Glu Trp Gly Ile Ser Ala Ala Thr Leu Arg	
195 200 205	
act tac caa aac tac ctt aag aac tac act act gag tac tct aac tac	671
Thr Tyr Gln Asn Tyr Leu Lys Asn Tyr Thr Thr Glu Tyr Ser Asn Tyr	
210 215 220	
tgc att aac act tac caa act gct ttc agg ggt ctt aac act agg ctt	719
Cys Ile Asn Thr Tyr Gln Thr Ala Phe Arg Gly Leu Asn Thr Arg Leu	
225 230 235	
cat gat atg ctt gag ttc agg act tac atg ttc ctt aac gtt ttc gag	767
His Asp Met Leu Glu Phe Arg Thr Tyr Met Phe Leu Asn Val Phe Glu	
240 245 250 255	
tac gtt tct att tgg tct ctt ttc aag tac cag tct ctt ctt gtt tct	815
Tyr Val Ser Ile Trp Ser Leu Phe Lys Tyr Gln Ser Leu Leu Val Ser	
260 265 270	
tct ggt gct aac ctt tac gct tct ggt tct ggt cct caa caa act caa	863
Ser Gly Ala Asn Leu Tyr Ala Ser Gly Ser Gly Pro Gln Gln Thr Gln	
275 280 285	
tct ttc act tct caa gac tgg cct ttc ctt tac tct ctt ttc caa gtt	911
Ser Phe Thr Ser Gln Asp Trp Pro Phe Leu Tyr Ser Leu Phe Gln Val	
290 295 300	
aac tct aac tac gtt ctt aac ggt ttc tct ggt gct agg ctt act caa	959
Asn Ser Asn Tyr Val Leu Asn Gly Phe Ser Gly Ala Arg Leu Thr Gln	
305 310 315	
act ttc cct aac atc ggt ggt ctt cct ggt act act act act cat gct	1007
Thr Phe Pro Asn Ile Gly Gly Leu Pro Gly Thr Thr Thr Thr His Ala	
320 325 330 335	
ctt ctt gct gct agg gtt aac tac tct ggt ggt gtt tct tct ggt gat	1055
Leu Leu Ala Ala Arg Val Asn Tyr Ser Gly Gly Val Ser Ser Gly Asp	
340 345 350	
atc ggt gct gtt ttc aac cag aac ttc tct tgc tct act ttc ctt cct	1103
Ile Gly Ala Val Phe Asn Gln Asn Phe Ser Cys Ser Thr Phe Leu Pro	
355 360 365	
cct ctt ctt act cct ttc gtt agg tct tgg ctt gat tct ggt tct gat	1151
Pro Leu Leu Thr Pro Phe Val Arg Ser Trp Leu Asp Ser Gly Ser Asp	
370 375 380	
agg ggt ggt gtt aac act gtt act aac tgg caa act gag tct ttc gag	1199
Arg Gly Gly Val Asn Thr Val Thr Asn Trp Gln Thr Glu Ser Phe Glu	
385 390 395	
tct act ctt ggt ctt agg tgc ggt gct ttc act gct agg ggt aac tct	1247
Ser Thr Leu Gly Leu Arg Cys Gly Ala Phe Thr Ala Arg Gly Asn Ser	
400 405 410 415	
aac tac ttc cct gat tac ttc att agg aac att tct ggt gtt cct ctt	1295

Asn Tyr Phe Pro Asp Tyr Phe Ile Arg Asn Ile Ser Gly Val Pro Leu	
420 425 430	
gtt gtt agg aac gag gat ctt agg agg cct ctt cat tac aac gag att	1343
Val Val Arg Asn Glu Asp Leu Arg Arg Pro Leu His Tyr Asn Glu Ile	
435 440 445	
agg aac att gag tct cct tct ggt act cct ggt ggt ctt agg gct tac	1391
Arg Asn Ile Glu Ser Pro Ser Gly Thr Pro Gly Gly Leu Arg Ala Tyr	
450 455 460	
atg gtt tct gtt cat aac agg aag aac aac atc tac gct gtt cat gag	1439
Met Val Ser Val His Asn Arg Lys Asn Asn Ile Tyr Ala Val His Glu	
465 470 475	
aac ggt act atg att cat ctt gct cct gag gat tac acc ggt ttc acc	1487
Asn Gly Thr Met Ile His Leu Ala Pro Glu Asp Tyr Thr Gly Phe Thr	
480 485 490 495	
atc tcc ccc atc cac gcc acc cag gtc aat aat cag acc agg acc ttc	1535
Ile Ser Pro Ile His Ala Thr Gln Val Asn Asn Gln Thr Arg Thr Phe	
500 505 510	
atc tcc gag aag ttc ggc aac cag ggc gac tcc ctg agg ttc gag cag	1583
Ile Ser Glu Lys Phe Gly Asn Gln Gly Asp Ser Leu Arg Phe Glu Gln	
515 520 525	
tcc aac acc acc gcc agg tac acc ctg agg ggc aac ggc aac tcc tac	1631
Ser Asn Thr Thr Ala Arg Tyr Thr Leu Arg Gly Asn Gly Asn Ser Tyr	
530 535 540	
aac ctg tac ctc agg gtg tcc tcc ctc ggc aac tcc acc atc agg gtc	1679
Asn Leu Tyr Leu Arg Val Ser Ser Leu Gly Asn Ser Thr Ile Arg Val	
545 550 555	
acc atc aac ggc agg gtg tac acc gcc tcc aac gtg aac acc acc acc	1727
Thr Ile Asn Gly Arg Val Tyr Thr Ala Ser Asn Val Asn Thr Thr Thr	
560 565 570 575	
aac aac gac ggc gtc aac gac aac ggc gct agg ttc ctg gac atc aac	1775
Asn Asn Asp Gly Val Asn Asp Asn Gly Ala Arg Phe Leu Asp Ile Asn	
580 585 590	
atg ggc aac gtc gtg gcc tcc gac aac acc aac gtg ccc ctg gac atc	1823
Met Gly Asn Val Val Ala Ser Asp Asn Thr Asn Val Pro Leu Asp Ile	
595 600 605	
aac gtg aca ttt aac tcc ggc acc cag ttc gag ctg atg aac atc atg	1871
Asn Val Thr Phe Asn Ser Gly Thr Gln Phe Glu Leu Met Asn Ile Met	
610 615 620	
ttc gtg cca act aac ctc cca ccc atc tac tgagctagc	1910
Phe Val Pro Thr Asn Leu Pro Pro Ile Tyr	
625 630	

<210> 8
 <211> 633
 <212> PRT
 <213> Unknown

<220>

<223> Artificial Sequence

<400> 8

Met Ala Asn Asn Val Leu Asn Asn Gly Arg Thr Thr Ile Cys Asp Ala
1 5 10 15

Tyr Asn Val Val Ala His Asp Pro Phe Ser Phe Glu His Lys Ser Leu
20 25 30

Asp Thr Ile Arg Lys Glu Trp Met Glu Trp Lys Arg Thr Asp His Ser
35 40 45

Leu Tyr Val Ala Pro Ile Val Gly Thr Val Ser Ser Phe Leu Leu Lys
50 55 60

Lys Val Gly Ser Leu Ile Gly Lys Arg Ile Leu Ser Glu Leu Trp Gly
65 70 75 80

Leu Ile Phe Pro Ser Gly Ser Thr Asn Leu Met Gln Asp Ile Leu Arg
85 90 95

Glu Thr Glu Gln Phe Leu Asn Gln Arg Leu Asn Thr Asp Thr Leu Ala
100 105 110

Arg Val Asn Ala Glu Leu Glu Gly Leu Gln Ala Asn Ile Arg Glu Phe
115 120 125

Asn Gln Gln Val Asp Asn Phe Leu Asn Pro Thr Gln Asn Pro Val Pro
130 135 140

Leu Ser Ile Thr Ser Ser Val Asn Thr Met Gln Gln Leu Phe Leu Asn
145 150 155 160

Arg Leu Pro Gln Phe Arg Val Gln Gly Tyr Gln Leu Leu Leu Leu Pro
165 170 175

Leu Phe Ala Gln Ala Ala Asn Met His Leu Ser Phe Ile Arg Asp Val
180 185 190

Val Leu Asn Ala Asp Glu Trp Gly Ile Ser Ala Ala Thr Leu Arg Thr
195 200 205

Tyr Gln Asn Tyr Leu Lys Asn Tyr Thr Thr Glu Tyr Ser Asn Tyr Cys
210 215 220

Ile Asn Thr Tyr Gln Thr Ala Phe Arg Gly Leu Asn Thr Arg Leu His
 225 230 235 240

Asp Met Leu Glu Phe Arg Thr Tyr Met Phe Leu Asn Val Phe Glu Tyr
 245 250 255

Val Ser Ile Trp Ser Leu Phe Lys Tyr Gln Ser Leu Leu Val Ser Ser
 260 265 270

Gly Ala Asn Leu Tyr Ala Ser Gly Ser Gly Pro Gln Gln Thr Gln Ser
 275 280 285

Phe Thr Ser Gln Asp Trp Pro Phe Leu Tyr Ser Leu Phe Gln Val Asn
 290 295 300

Ser Asn Tyr Val Leu Asn Gly Phe Ser Gly Ala Arg Leu Thr Gln Thr
 305 310 315 320

Phe Pro Asn Ile Gly Gly Leu Pro Gly Thr Thr Thr Thr His Ala Leu
 325 330 335

Leu Ala Ala Arg Val Asn Tyr Ser Gly Gly Val Ser Ser Gly Asp Ile
 340 345 350

Gly Ala Val Phe Asn Gln Asn Phe Ser Cys Ser Thr Phe Leu Pro Pro
 355 360 365

Leu Leu Thr Pro Phe Val Arg Ser Trp Leu Asp Ser Gly Ser Asp Arg
 370 375 380

Gly Gly Val Asn Thr Val Thr Asn Trp Gln Thr Glu Ser Phe Glu Ser
 385 390 395 400

Thr Leu Gly Leu Arg Cys Gly Ala Phe Thr Ala Arg Gly Asn Ser Asn
 405 410 415

Tyr Phe Pro Asp Tyr Phe Ile Arg Asn Ile Ser Gly Val Pro Leu Val
 420 425 430

Val Arg Asn Glu Asp Leu Arg Arg Pro Leu His Tyr Asn Glu Ile Arg
 435 440 445

Asn Ile Glu Ser Pro Ser Gly Thr Pro Gly Gly Leu Arg Ala Tyr Met
 450 455 460

Val Ser Val His Asn Arg Lys Asn Asn Ile Tyr Ala Val His Glu Asn

465 470 475 480
 Gly Thr Met Ile His Leu Ala Pro Glu Asp Tyr Thr Gly Phe Thr Ile
 485 490 495
 Ser Pro Ile His Ala Thr Gln Val Asn Asn Gln Thr Arg Thr Phe Ile
 500 505 510
 Ser Glu Lys Phe Gly Asn Gln Gly Asp Ser Leu Arg Phe Glu Gln Ser
 515 520 525
 Asn Thr Thr Ala Arg Tyr Thr Leu Arg Gly Asn Gly Asn Ser Tyr Asn
 530 535 540
 Leu Tyr Leu Arg Val Ser Ser Leu Gly Asn Ser Thr Ile Arg Val Thr
 545 550 555 560
 Ile Asn Gly Arg Val Tyr Thr Ala Ser Asn Val Asn Thr Thr Thr Asn
 565 570 575
 Asn Asp Gly Val Asn Asp Asn Gly Ala Arg Phe Leu Asp Ile Asn Met
 580 585 590
 Gly Asn Val Val Ala Ser Asp Asn Thr Asn Val Pro Leu Asp Ile Asn
 595 600 605
 Val Thr Phe Asn Ser Gly Thr Gln Phe Glu Leu Met Asn Ile Met Phe
 610 615 620
 Val Pro Thr Asn Leu Pro Pro Ile Tyr
 625 630

<210> 9
 <211> 1910
 <212> DNA
 <213> Unknown

<220>

<223> artificial cry2Ae DNA sequence for expression in corn

<400> 9

ccatggctaa caacgtgctg aacaacggca ggaccaccat ctgcgatgca tacaacgtgg 60
 tggcccacga cccattcagc ttcgagcaca agagcctgga caccatccgc aaggagtgga 120
 tggagtggaa gcgcaccgac cacagcctgt acgtggcccc tatcgtgggc accgtgagca 180
 gcttctgtct gaagaagggtg ggcagcctga tcggcaagag gatcctgagc gagctgtggg 240
 gcctgatctt cccaagcggc agcaccaacc tgatgcagga catcctgagg gagaccgagc 300

agttcctgaa ccagcgctg aacaccgaca ccttggtctg cgtgaacgcc gagctggagg	360
gcctccaggc caacatcagg gaattcaacc agcaggtgga caacttcctg aaccaaccc	420
agaacccagt gccactgagc atcaccagca gcgtgaacac catgcagcag ctgttcctga	480
accgcctgcc acagttccgc gtgcagggct accagctgct gctgctgcca ctgttcgccc	540
aggctgccaa catgcaccta agcttcatcc gcgacgtggt gctgaacgcc gacgagtggg	600
gcatcagcgc tgccaccctg cgcacctacc agaactacct gaagaactac accaccgagt	660
acagcaacta ctgcatcaac acctaccaga ccgccttcag gggcctgaac accaggtgc	720
acgacatgct ggagttccgc acctacatgt tcctgaacgt gttcgagtac gtgagcatct	780
ggagcctgtt caagtaccag agcctgctgg tgagcagcgg tgccaacctg tacgccagcg	840
gcagcggctc acagcagacc cagagcttca ccagccagga ctggcccttc ctgtacagcc	900
tgttccaggc gaacagcaac tacgtgctga acggcttcag cggtgccagg ctgaccaga	960
ccttccaaa catcggaggc ctgccaggca ccaccaccac ccacgcctg ctggctgcca	1020
gggtgaacta cagcgggtggc gtgagcagcg gcgatatcgg cgtgtgttc aaccagaact	1080
tcagctgcag caccttcctg ccaccactgc tgacccatt cgtgcgcagc tggctggaca	1140
gcggcagcga caggggtggc gtgaacaccg tgaccaactg gcagaccgag agcttcgaga	1200
gcaccctggg cctgcgctgc ggtgccttca ccgccagggg caacagcaac tacttcccag	1260
actacttcat ccgcaacatc agcggcgtgc cactggtggt gcgcaacgag gacctgcga	1320
ggccactgca ctacaacgag atccgcaaca tcgagagccc aagcggcacc ccaggaggcc	1380
tgagggccta catggtgagc gtgcacaacc gcaagaacaa catctacgcc gtgcacgaga	1440
acggcaccat gatccacctg gcccagagg actacaccgg ttccaccatc tccccatcc	1500
acgccaccca ggtcaataat cagaccagga ccttcatctc cgagaagttc ggcaaccagg	1560
gcgactccct gaggttcgag cagtccaaca ccaccgccag gtacaccctg aggggcaacg	1620
gcaactccta caacctgtac ctcaggggtgt cctccctcgg caactccacc atcaggggtca	1680
ccatcaacgg caggggtgtac accgcctcca acgtgaacac caccaccaac aacgacggcg	1740
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